

SEQUENCE LISTING

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Wong, Chi-Wai
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<120> Methods of Diagnosing & Treating Diabetes and Insulin Resistance

<130> 016325-013600US

<140> US 10/516,780
<141> 2004-12-03

<150> US 60/386,521
<151> 2002-06-05

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<150> US 60/387,301
<151> 2002-06-07

<150> WO PCT/US03/18046
<151> 2003-06-05

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<170> PatentIn Ver. 2.1

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<223> Fritz

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Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Asp Asn
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 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
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 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
 115 120 125
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 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
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 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
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 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
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 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
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<213> Mus musculus

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<223> mouse Fritz (frizzled-related protein)

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35 40 45

Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60

Ala Ile Leu Ala Met Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80

Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
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Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110

Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
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Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu Pro Val Tyr Asp Arg
130 135 140

Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
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Phe Pro Met Asp Ser Ser Thr Gly His Cys Arg Gly Ala Ser Ser Glu
165 170 175

Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190

Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Met
195 200 205

Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220

Ala Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Thr
225 230 235 240

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
245 250 255

Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
260 265 270

Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
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Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
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Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
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Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
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Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
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Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
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Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
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Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
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Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
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Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
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Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
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Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Leu Asn Thr Glu
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Lys Gln Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
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Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Tyr Thr Arg
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Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
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Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
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Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
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 Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
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 Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
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 Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
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 Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
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 Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
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 485 490 495
 Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala
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 Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser
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35 40 45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
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Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
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Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
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Glu Asp Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
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Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
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Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
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Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu
 225 230 235 240

Lys Gln Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
 245 250 255

Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Tyr Thr Arg
 260 265 270

Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
 275 280 285

Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
 290 295 300

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
 305 310 315 320

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
 325 330 335

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
 340 345 350

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
 355 360 365

Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
 370 375 380

Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
 385 390 395 400

Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
 405 410 415
 Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
 420 425 430
 Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
 435 440 445
 Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
 450 455 460
 Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly
 465 470 475 480
 Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp
 485 490 495
 Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala
 500 505 510
 Lys Glu Leu Leu Gln Val Arg Lys Leu Arg Phe Gln Val Phe Ser Asn
 515 520 525
 Phe Ser Met Ile Ala Ala Ser Ile Pro Glu Asp Cys Gln Ala Pro Leu
 530 535 540
 Gln Pro His Ser Thr Asp Cys Cys Ser
 545 550

<210> 9
 <211> 1347
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> human p21 activated kinase 1B (PAK1B) new splice
 variant

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 cctccaaacc cagaggagaa gaaaaagaag gaccgatttt accgatccat tttacctgga 180
 gataaaaacaa ataaaaagaa agagaaaagag cggccagaga tttctctccc ttcagattt 240
 gaacacacaa ttcatgtcgg ttttcatgtcgt gtcacagggg agtttacggg aatgccagag 300
 cagtgggccc gcttgcttca gacatcaa atcactaagt cggagcagaa gaaaaacccg 360
 caggctgttc tggatgtgtt ggagtttac aactcgaaga agacatccaa cagccagaaa 420
 tacatgagct ttacagataa gtcagctgag gattacaatt cttctaattgc cttgaatgtg 480
 aaggctgtgt ctgagactcc tgcagtgcctt ccagtttcag aagatgagga tgatgtatgat 540
 gatgatgcta cccaccacc agtgattgtcc ccacgcccag agcacacaaa atctgtggcc 600
 attaaggcaga tgaatcttca gcagcagccc aagaaaagagc tgattattaa tgagatcctg 660
 gtcatgaggg aaaacaagaa cccaaacatt gtgaattact tggacagttt cctcgtggga 720
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 ggaatggatg gctctgtcaa gctaactgac tttggattct gtgcacagat aaccccgag 960
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ctgaaccgct gtctcggat ggatgtggag aagagagggtt cagctaaaga gctgctacag 1260
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aaggaggcaa caaagaacaa tcactaa 1347

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<211> 449
<212> PRT
<213> Homo sapiens

<220>
<223> human p21 activated kinase 1B (PAK1B) new splice
variant

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Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Ala Gly
20 25 30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
35 40 45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
50 55 60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
65 70 75 80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
85 90 95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
100 105 110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
115 120 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
130 135 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn
145 150 155 160

Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
165 170 175

Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
180 185 190

Arg Pro Glu His Thr Lys Ser Val Ala Ile Lys Gln Met Asn Leu Gln
195 200 205

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
210 215 220

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
225 230 235 240

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
 245 250 255
 Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
 260 265 270
 Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
 275 280 285
 Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
 290 295 300
 Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
 305 310 315 320
 Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
 325 330 335
 Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
 340 345 350
 Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
 355 360 365
 Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly
 370 375 380
 Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp
 385 390 395 400
 Phe Leu Asn Arg Cys Leu Gly Met Asp Val Glu Lys Arg Gly Ser Ala
 405 410 415
 Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser
 420 425 430
 Ser Leu Thr Pro Leu Ile Ala Ala Lys Glu Ala Thr Lys Asn Asn
 435 440 445

His

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<210> 11
<211> 1977
<212> DNA
<213> Mus musculus

<220>
<223> mouse p21 (CDKN1A)-activated kinase 1B (PAK1B)
      cDNA

<220>
<221> CDS
<222> (190)..(1827)
<223> PAK1B

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gtggtagaca tgtcaaataa cggcgttagac atccaggaca aaccccccagc ccctccgatg 240
  
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 atcttacctg gagataaaac aaataaaaag agggagaagg agcgaccaga gatttcttt 420
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 ttctatgaaa taaacactt gttcgaaac tccgacacctt catgtcctct tctcctttcc 1920
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<210> 12
 <211> 545
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse p21 (CDKN1A)-activated kinase 1B (PAK1B)

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Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Thr Gly
 20 25 30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
 35 40 45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
 50 55 60

Asn Lys Lys Arg Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
 65 70 75 80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
 85 90 95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
 100 105 110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
 115 120 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Lys Lys Tyr Met Ser
 130 135 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Thr Leu Asn
 145 150 155 160

Val Lys Thr Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
 165 170 175

Asp Glu Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
 180 185 190

Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
 195 200 205

Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
 210 215 220

Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu
 225 230 235 240

Lys Gln Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
 245 250 255

Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Pro
 260 265 270

Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
 275 280 285

Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
 290 295 300

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
 305 310 315 320

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
 325 330 335

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
 340 345 350

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
 355 360 365

Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
 370 375 380

Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
 385 390 395 400

Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
 405 410 415

Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
 420 425 430

Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp
435 440 445

Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr
450 455 460

Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly
465 470 475 480

Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp
485 490 495

Phe Leu Gln Cys Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala
500 505 510

Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser
515 520 525

Ser Leu Thr Pro Leu Met His Ala Ala Lys Glu Ala Thr Lys Asn Asn
530 535 540

His
545

<210> 13
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<212> DNA
<213> Rattus norvegicus

<220>
<223> rat p21 (CDKN1A)-activated kinase 1B (PAK1B) cDNA

<220>
<221> CDS
<222> (389)..(2023)
<223> PAK1B

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<210> 14
 <211> 544
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat p21 (CDKN1A)-activated kinase 1B (PAK1B)

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Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Pro Gly
 20 25 30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
 35 40 45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Ala Gly Asp Lys Thr
 50 55 60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
 65 70 75 80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
 85 90 95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
 100 105 110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
 115 120 125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
 130 135 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Thr Leu Asn
 145 150 155 160

Val Lys Thr Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
 165 170 175

 Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro Arg
 180 185 190

 Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro Leu
 195 200 205

 Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro Thr
 210 215 220

 Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu Lys
 225 230 235 240

 Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys Leu
 245 250 255

 Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Arg Phe
 260 265 270

 Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met Asp
 275 280 285

 Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln Gln
 290 295 300

 Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg Glu
 305 310 315 320

 Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val Gly
 325 330 335

 Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu Thr
 340 345 350

 Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala Val
 355 360 365

 Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln Val
 370 375 380

 Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp Gly
 385 390 395 400

 Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro Glu
 405 410 415

 Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala Pro
 420 425 430

 Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp Ser
 435 440 445

 Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr Leu
 450 455 460

 Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly Thr
 465 470 475 480

Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp Phe
485 490 495

Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala Lys
500 505 510

Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser Ser
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Leu Thr Pro Leu Ile Ala Ala Ala Lys Glu Ala Thr Lys Asn Asn His
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<212> DNA
<213> Homo sapiens

<220>
<223> human SPUVE serine protease 23 cDNA

<220>
<221> CDS
<222> (121)..(1272)
<223> SPUVE

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<210> 16
<211> 383
<212> PRT
<213> Homo sapiens

<220>

<223> human SPUVE serine protease 23

<400> 16

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Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
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Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
35 40 45

Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser
50 55 60

Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu
65 70 75 80

Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
85 90 95

Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
100 105 110

Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
115 120 125

Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
130 135 140

Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
145 150 155 160

Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys
165 170 175

Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
180 185 190

Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
195 200 205

Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
210 215 220

Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
225 230 235 240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
245 250 255

Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
260 265 270

Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
275 280 285

Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
290 295 300

Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val
305 310 315 320

Tyr Val Arg Met Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile
325 330 335

Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
340 345 350

Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
355 360 365

Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly
370 375 380

<210> 17

<211> 1936

<212> DNA

<213> Mus musculus

<220>

<223> mouse SPUVE serine protease 23 cDNA

<220>

<221> CDS

<222> (170)..(1318)

<223> SPUVE

<400> 17

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cccgccggctc ttcatccctc ttgtcctgtct ctgtgtgttgc atgcaggta gtccttacac 240
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aaaaaaaaaaa aaaaaaa 1936

<210> 18
<211> 382
<212> PRT
<213> Mus musculus

<220>
<223> mouse SPUVE serine protease 23

<400> 18
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Phe Met Gln Val Ser Pro Tyr Thr Val Pro Trp Lys Pro Thr Trp Pro
20 25 30
Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala
35 40 45
Lys Ala Asp Phe Asp Ala Lys Ala Lys Leu Glu Val Ser Ser Ser Cys
50 55 60
Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu Ala
65 70 75 80
Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr
85 90 95
Glu Thr Arg Val Gly Ile Tyr Ile Leu Ser Asn Gly Glu Gly Arg Ala
100 105 110
Arg Gly Arg Asp Ser Glu Ala Thr Gly Arg Ser Arg Arg Lys Arg Gln
115 120 125
Ile Tyr Gly Tyr Asp Gly Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu
130 135 140
Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr
145 150 155 160
Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile
165 170 175
His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly
180 185 190
Phe Leu Lys Pro Lys Tyr Lys Asp Gly Ala Gly Gly Asp Asn Ser Ser
195 200 205
Ser Ser Ala Met Pro Asp Lys Met Lys Phe Gln Trp Ile Arg Val Lys
210 215 220
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile
225 230 235 240
Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys
245 250 255

Arg Gln Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro
260 265 270

Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn
 275 280 285

Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu
290 295 300

Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val Tyr
 305 310 315 320

Val Arg Met Trp Lys Arg Pro Gln Gln Lys Trp Glu Arg Lys Ile Ile
 325 330 335

Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln
340 345 350

Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile
355 360 365

Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly
370 375 380

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<210> 19
<211> 827
<212> DNA
<213> Homo sapiens
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<220>
<223> human similar to natural killer cell transcript 4
(NK4) cDNA

<220>
<221> CDS
<222> (59)..(625)
<223> NK4

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catagaaaaga ttttatgata aaatgcaaaaa tgccagaatca ggacgtggac aggtgtatgtc 180
gagcctggca gagctggagg acgacttcaa agagggctac ctggagacag tggcggctta 240
ttatgaggag cagcaccaggc agctcactcc tctacttgaa aaagaaaagag atggattacg 300
gtgccgaggc aacagatccc ctgtcccgga tggttggaggat cccgcaacccg aggagctgg 360
ggagagctt tgtgacaagg tcatgagatg gttccagggcc atgctgcagc ggctgcagac 420
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gcaggccctc tgaaaacagt tccagagttt ctgctgctct ctgtcagagc tcttcatgtc 540
ctctttccag tcc tacggag cccacgggg ggacaaggag gagctgacac cccagaagtg 600
ctctgaaccc caatcctcaa aatgaagata ctgacaccac ctttgcctc cccgtcaccg 660
cgcacccacc ctgacccctc cctcagctgt cctgtgcccc gcctctccc gcacactcag 720
tccccctgcc tggcgttccct gccgcagctc tgacctggtg ctgtcgcctc ggcatcttaa 780
taaaaacctqc ttataacttcc ctqaaaaaaaaaaaaaaa aaaaaaaaaa 827

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<210> 20
<211> 188
<212> PRT
<213> Homo sapiens
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<220>
 <223> human similar to natural killer cell transcript 4
 (NK4)

<400> 20
 Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
 1 5 10 15

Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
 20 25 30

Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
 35 40 45

Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
 50 55 60

Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
 65 70 75 80

Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
 85 90 95

Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
 100 105 110

Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
 115 120 125

Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
 130 135 140

Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
 145 150 155 160

Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
 165 170 175

Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
 180 185

<210> 21
 <211> 2254
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human Protein C inhibitor (PCI) cDNA

<220>
 <221> CDS
 <222> (140)..(1360)
 <223> PCI

<400> 21
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 agaacaaga aca gccacca tgcagcttt cctcctcttg tgcctggc ttctcagccc 180
 tcagggggcc tcccttcacc gccaccaccc cgggagatg aagaagagag tcgaggacct 240
 ccatgttaggt gccacggtgg cccccagcag cagaaggacac ttacaccttgc acctctacag 300

ggccttggct tccgctgccc ccagccagaa catcttcttc tcccctgtga gcatctccat 360
 gaggcctggcc atgctctccc tgggggctgg gtccagcaca aagatgcaga tcctggaggg 420
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 cctgcatggg aaaaatgttg gaatgggagt ctgaaaatggg gctactgttt cagtcctaac 1860
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 tagttataat ctgatgggccc tggctggag tggagaagg gaagcccttt gcaaataatgta 2160
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 aagcatttttgc caaacaaaaaa aaaaaaaaaa aaaa 2254

<210> 22
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human Protein C inhibitor (PCI)

<400> 22
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Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys Arg Val Glu
 20 25 30

Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg Arg Asp Phe
 35 40 45

Thr Phe Asp Leu Tyr Arg Ala Leu Ala Ser Ala Ala Pro Ser Gln Asn
 50 55 60

Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala Met Leu Ser
 65 70 75 80

Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu Gly Leu Gly
 85 90 95

Leu Asn Leu Gln Lys Ser Ser Glu Lys Glu Leu His Arg Gly Phe Gln
 100 105 110

Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe Gln Leu Ser
 115 120 125

Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu Gln Asp Thr
 130 135 140

Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr Phe Pro Thr
 145 150 155 160

Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn Asp Tyr Val
 165 170 175

Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys Asn Leu Asp
 180 185 190

Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe Lys Ala Lys
 195 200 205

Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln Asp Phe Tyr
 210 215 220

Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser Arg Glu Asp
 225 230 235 240

Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg Val Val Gly
 245 250 255

Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu Pro Ser Glu
 260 265 270

Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys Thr Leu Arg
 275 280 285

Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu Tyr Leu Pro
 290 295 300

Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val Leu Pro Ser
 305 310 315 320

Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu Ser Gly Ile
 325 330 335

Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His Lys Ala Val
 340 345 350

Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala Thr Gly Thr
 355 360 365

Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg Leu Val Phe
 370 375 380

Asn Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile Leu Phe Leu
 385 390 395 400

Gly Lys Val Asn Arg Pro
 405

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<210> 23
<211> 2125
<212> DNA
<213> Mus musculus

<220>
<223> mouse Protein C inhibitor (PCI), serine (or
      cysteine) proteinase inhibitor, clade A, member 5
      (Serpina5) cDNA

<220>
<221> CDS
<222> (125) .. (1342)
<223> PCI

<400> 23
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cacagttgca agatgtgttgc ttgtctcat ccttcatcat tgacactgac cctaaagagg 1560
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ctggcaataa aggcattttt caaag 2125

<210> 24
<211> 405
<212> PRT
<213> Mus musculus

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<220>

<223> mouse Protein C inhibitor (PCI), serine (or
cysteine) proteinase inhibitor, clade A, member 5
(Serpina5)

<400> 24

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Val Ala Ser Arg Arg His Ser His Ser Lys Lys Lys Lys Ala Lys Glu
20 25 30

Ser Ser Val Gly Ala Val Gly Pro Pro Ser Ser Lys Asp Phe Ala Phe
35 40 45

Arg Leu Tyr Arg Ala Leu Ala Ser Glu Ser Pro Gly Gln Asn Val Phe
50 55 60

Phe Ser Pro Leu Ser Val Ser Met Ser Leu Gly Met Leu Ser Leu Gly
65 70 75 80

Ala Gly Leu Lys Thr Lys Thr Gln Ile Leu Asp Gly Leu Gly Leu Ser
85 90 95

Leu Gln Gln Gly Gln Glu Asp Lys Leu His Lys Gly Phe Gln Gln Leu
100 105 110

Leu Gln Arg Phe Arg Gln Pro Ser Asp Gly Leu Gln Leu Ser Leu Gly
115 120 125

Ser Ala Leu Phe Lys Asp Pro Ala Val His Ile Arg Asp Asp Phe Leu
130 135 140

Ser Ala Met Lys Thr Leu Tyr Met Ser Asp Thr Phe Ser Thr Asn Phe
145 150 155 160

Gly Asn Pro Glu Ile Ala Lys Lys Gln Ile Asn Asn Tyr Val Ala Lys
165 170 175

Gln Thr Lys Gly Lys Ile Val Asp Leu Ile Lys Asp Leu Asp Ser Thr
180 185 190

His Val Met Ile Val Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Gln
195 200 205

Thr Ala Phe Ser Glu Thr Asn Thr His Lys Met Asp Phe His Val Thr
210 215 220

Pro Lys Lys Thr Ile Arg Val Pro Met Met Asn Arg Glu Asp Glu Tyr
225 230 235 240

Ser Tyr Tyr Leu Asp Gln Asn Ile Ser Cys Thr Val Val Gly Ile Pro
245 250 255

Tyr Gln Gly Asn Ala Ile Ala Leu Phe Ile Leu Pro Ser Glu Gly Lys
260 265 270

Met Lys Gln Val Glu Asp Gly Leu Asp Glu Arg Thr Leu Arg Asn Trp
275 280 285

Leu Lys Met Phe Thr Lys Arg Arg Leu Asp Leu Tyr Leu Pro Lys Phe
290 295 300

Ser Ile Glu Ala Thr Tyr Lys Leu Glu Asn Val Leu Pro Lys Leu Gly
305 310 315 320

Ile Gln Asp Val Phe Thr Thr His Ala Asp Leu Ser Gly Ile Thr Asp
325 330 335

His Thr Asn Ile Lys Leu Ser Glu Met Val His Lys Ser Met Met Glu
340 345 350

Val Glu Glu Ser Gly Thr Thr Ala Ala Ala Ile Thr Gly Ala Ile Phe
355 360 365

Thr Phe Arg Ser Ala Arg Pro Ser Ser Leu Lys Ile Glu Phe Thr Arg
370 375 380

Pro Phe Leu Leu Thr Leu Met Glu Asp Ser His Ile Leu Phe Val Gly
385 390 395 400

Lys Val Thr Arg Pro
405

<210> 25

<211> 2035

<212> DNA

<213> Rattus norvegicus

<220>

<223> rat Protein C inhibitor (PCI), serine (or
cysteine) proteinase inhibitor, clade A, member 5
(Serpina5) cDNA

<220>

<221> CDS

<222> (48)..(1268)

<223> PCI

<400> 25

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 <212> PRT
 <213> Rattus norvegicus

<220>
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 cysteine) proteinase inhibitor, clade A, member 5
 (Serpina5)

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Glu Ser Ser Val Gly Ala Val Gly Thr Ser Arg Ser Arg Asp Phe Ala
 35 40 45

Phe Arg Leu Tyr Arg Ala Leu Ala Ser Glu Ala Pro Gly Gln Asn Val
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Phe Phe Ser Pro Met Ser Val Ser Met Ser Leu Gly Met Leu Ser Leu
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Gly Ser Gly Leu Lys Thr Lys Ala Gln Ile Leu Glu Gly Leu Gly Leu
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Ser Leu Gln Gln Gly Gln Glu Asp Met Leu His Lys Gly Phe Gln Gln
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Leu Leu Gln Gln Phe Ser Gln Pro Ser Asp Gly Leu Gln Leu Ser Leu
 115 120 125

Gly Ser Ala Leu Phe Thr Asp Pro Ala Val His Ile Arg Asp His Phe
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Leu Ser Ala Met Lys Thr Leu Tyr Met Ser Asp Met Phe Ser Thr Asn
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Phe Gly Asn Pro Glu Ser Ala Lys Lys Gln Ile Asn Asp Tyr Val Ala
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Lys Lys Thr Asn Gly Lys Ile Val Asp Leu Ile Lys Asp Leu Asp Ser
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Thr His Val Met Val Val Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp
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Gln Thr Ala Phe Ser Ser Thr Asn Thr His Lys Met Asp Phe His Val
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Thr Pro Lys Lys Thr Ile Gln Val Pro Met Met Asn Arg Glu Asp Ile
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Tyr Ser Tyr Ile Leu Asp Gln Asn Ile Ser Cys Thr Val Val Gly Ile
245 250 255

Pro Tyr Gln Gly Asn Thr Phe Ala Leu Phe Ile Leu Pro Ser Glu Gly
260 265 270

Lys Met Lys Arg Val Glu Asp Gly Leu Asp Glu Arg Thr Leu Arg Asn
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Trp Leu Lys Met Phe Thr Lys Arg Gln Leu Asp Leu Tyr Leu Pro Lys
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Phe Ser Ile Glu Gly Thr Tyr Lys Leu Glu Lys Ile Leu Pro Lys Leu
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Gly Ile Gln Asp Ile Phe Thr Thr His Ala Asp Leu Ser Gly Leu Thr
325 330 335

Asp His Thr Asn Ile Lys Leu Ser Glu Met Val His Lys Ser Met Val
340 345 350

Glu Val Asp Glu Ser Gly Thr Thr Ala Ala Ala Ser Thr Gly Ile Leu
355 360 365

Phe Thr Leu Arg Ser Ala Arg Pro Ser Ser Leu Lys Val Glu Phe Thr
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Gly Lys Val Ile Gln Pro
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<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens

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 Asn Pro Arg Ala His Ser Ser Pro Gly Thr Pro Cys Ser Ser Arg Pro
 35 40 45

 Leu Pro Trp Ser Cys Arg Thr Ser Asn Arg Lys Ser Leu Ile Val Thr
 50 55 60

 Ser Ser Thr Ser Pro Thr Leu Pro Arg Pro His Ser Pro Leu His Gly
 65 70 75 80

 His Thr Gly Asn Ser Pro Leu Asp Ser Pro Arg Asn Phe Ser Pro Asn
 85 90 95

 Ala Pro Ala His Phe Ser Phe Val Pro Ala Arg Ser His Ser His Arg
 100 105 110

 Ala Asp Arg Thr Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser
 115 120 125

 Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys
 130 135 140

Ser Ser Gln Glu Lys Leu His Gln Leu Leu Phe Gln Pro Thr Ala Asp
 145 150 155 160

Glu Leu His Phe Leu Thr Lys His Phe Ser Thr Glu Ser Val Pro Asp
 165 170 175

Glu Glu Gly Arg Gln Ser Pro Ala Met Arg Pro Arg Ser Arg Ser Leu
 180 185 190

Ser Pro Gly Arg Ser Pro Val Ser Phe Asp Ser Glu Ile Ile Met Met
 195 200 205

Asn His Val Tyr Lys Glu Arg Phe Pro Lys Ala Thr Ala Gln Met Glu
 210 215 220

Glu Arg Leu Ala Glu Phe Ile Ser Ser Asn Thr Pro Asp Ser Val Leu
 225 230 235 240

Pro Leu Ala Asp Gly Ala Leu Ser Phe Ile His His Gln Val Ile Glu
 245 250 255

Met Ala Arg Asp Cys Leu Asp Lys Ser Arg Ser Gly Leu Ile Thr Ser
 260 265 270

Gln Tyr Phe Tyr Glu Leu Gln Glu Asn Leu Glu Lys Leu Leu Gln Asp
 275 280 285

Ala His Glu Arg Ser Glu Ser Ser Glu Val Ala Phe Val Met Gln Leu
 290 295 300

Val Lys Lys Leu Met Ile Ile Ile Ala Arg Pro Ala Arg Leu Leu Glu
 305 310 315 320

Cys Leu Glu Phe Asp Pro Glu Glu Phe Tyr His Leu Leu Glu Ala Ala
 325 330 335

Glu Gly His Ala Lys Glu Gly Gln Gly Ile Lys Cys Asp Ile Pro Arg
 340 345 350

Tyr Ile Val Ser Gln Leu Gly Leu Thr Arg Asp Pro Leu Glu Glu Met
 355 360 365

Ala Gln Leu Ser Ser Cys Asp Ser Pro Asp Thr Pro Glu Thr Asp Asp
 370 375 380

Ser Ile Glu Gly His Gly Ala Ser Leu Pro Ser Lys Lys Thr Pro Ser
 385 390 395 400

Glu Glu Asp Phe Glu Thr Ile Lys Leu Ile Ser Asn Gly Ala Tyr Gly
 405 410 415

Ala Val Phe Leu Val Arg His Lys Ser Thr Arg Gln Arg Phe Ala Met
 420 425 430

Lys Lys Ile Asn Lys Gln Asn Leu Ile Leu Arg Asn Gln Ile Gln Gln
 435 440 445

Ala Phe Val Glu Arg Asp Ile Leu Thr Phe Ala Glu Asn Pro Phe Val
 450 455 460

Val Ser Met Phe Cys Ser Phe Asp Thr Lys Arg His Leu Cys Met Val
 465 470 475 480
 Met Glu Tyr Val Glu Gly Gly Asp Cys Ala Thr Leu Leu Lys Asn Ile
 485 490 495
 Gly Ala Leu Pro Val Asp Met Val Arg Leu Tyr Phe Ala Glu Thr Val
 500 505 510
 Leu Ala Leu Glu Tyr Leu His Asn Tyr Gly Ile Val His Arg Asp Leu
 515 520 525
 Lys Pro Asp Asn Leu Leu Ile Thr Ser Met Gly His Ile Lys Leu Thr
 530 535 540
 Asp Phe Gly Leu Ser Lys Met Gly Leu Met Ser Leu Thr Thr Asn Leu
 545 550 555 560
 Tyr Glu Gly His Ile Glu Lys Asp Ala Arg Glu Phe Leu Asp Lys Gln
 565 570 575
 Val Cys Gly Thr Pro Glu Tyr Ile Ala Pro Glu Val Ile Leu Arg Gln
 580 585 590
 Gly Tyr Gly Lys Pro Val Asp Trp Trp Ala Met Gly Ile Ile Leu Tyr
 595 600 605
 Glu Phe Leu Val Gly Cys Val Pro Phe Phe Gly Asp Thr Pro Glu Glu
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 Leu Phe Gly Gln Val Ile Ser Asp Glu Ile Val Trp Pro Glu Gly Asp
 625 630 635 640
 Glu Ala Leu Pro Pro Asp Ala Gln Asp Leu Thr Ser Lys Leu Leu His
 645 650 655
 Gln Asn Pro Leu Glu Arg Leu Gly Thr Gly Ser Ala Tyr Glu Val Lys
 660 665 670
 Gln His Pro Phe Phe Thr Gly Leu Asp Trp Thr Gly Leu Leu Arg Gln
 675 680 685
 Lys Ala Glu Phe Ile Pro Gln Leu Glu Ser Glu Asp Asp Thr Ser Tyr
 690 695 700
 Phe Asp Thr Arg Ser Glu Arg Tyr His His Met Asp Ser Glu Asp Glu
 705 710 715 720
 Glu Glu Val Ser Glu Asp Gly Cys Leu Glu Ile Arg Gln Phe Ser Ser
 725 730 735
 Cys Ser Pro Arg Phe Asn Lys Val Tyr Ser Ser Met Glu Arg Leu Ser
 740 745 750
 Leu Leu Glu Glu Arg Arg Thr Pro Pro Pro Thr Lys Arg Ser Leu Ser
 755 760 765
 Glu Glu Lys Glu Asp His Ser Asp Gly Leu Ala Gly Leu Lys Gly Arg
 770 775 780

Asp Arg Ser Trp Val Ile Gly Ser Pro Glu Ile Leu Arg Lys Arg Leu
 785 790 795 800
 Ser Val Ser Glu Ser Ser His Thr Glu Ser Asp Ser Ser Pro Pro Met
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 Thr Val Arg Arg Cys Ser Gly Leu Leu Asp Ala Pro Arg Phe Pro
 820 825 830
 Glu Gly Pro Glu Glu Ala Ser Ser Thr Leu Arg Arg Gln Pro Gln Glu
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 Gly Ile Trp Val Leu Thr Pro Pro Ser Gly Glu Gly Val Ser Gly Pro
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 Val Thr Glu His Ser Gly Glu Gln Arg Pro Lys Leu Asp Glu Glu Ala
 865 870 875 880
 Val Gly Arg Ser Ser Gly Ser Ser Pro Ala Met Glu Thr Arg Gly Arg
 885 890 895
 Gly Thr Ser Gln Leu Ala Glu Gly Ala Thr Ala Lys Ala Ile Ser Asp
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 Glu Lys Arg Thr Ala Arg Pro Val Asn Lys Val Ile Lys Ser Ala Ser
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 Ala Thr Ala Leu Ser Leu Leu Ile Pro Ser Glu His His Thr Cys Ser
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 Pro Leu Ala Ser Pro Met Ser Pro His Ser Gln Ser Ser Asn Pro Ser
 965 970 975
 Ser Arg Asp Ser Ser Pro Ser Arg Asp Phe Leu Pro Ala Leu Gly Ser
 980 985 990
 Met Arg Pro Pro Ile Ile Ile His Arg Ala Gly Lys Lys Tyr Gly Phe
 995 1000 1005
 Thr Leu Arg Ala Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr
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 Val His Gly Leu Val His Thr Glu Val Val Glu Leu Ile Leu Lys Ser
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 Gly Asn Lys Val Ala Ile Ser Thr Thr Pro Leu Glu Asn Thr Ser Ile
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 1090 1095 1100

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 Gly Pro Gly Ser Pro Thr His Ser His Ser Leu Ser Pro Arg Ser Pro
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 Thr Gln Gly Tyr Arg Val Thr Pro Asp Ala Val His Ser Val Gly Gly
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Thr Gly Pro Ala Gly Pro Glu Gly Lys Glu Gln Asp Val Val Thr Gly
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Val Ser Pro Leu Leu Phe Arg Lys Leu Ser Asn Pro Asp Ile Phe Ser
 65 70 75 80

Ser Thr Gly Lys Val Lys Leu Gln Arg Gln Leu Ser Gln Asp Asp Cys
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Lys Leu Trp Arg Gly Asn Leu Ala Ser Ser Leu Ser Gly Lys Gln Leu
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Leu Pro Leu Ser Ser Ser Val His Ser Ser Val Gly Gln Val Thr Trp
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Gln Ser Ser Gly Glu Ala Ser Asn Leu Val Arg Met Arg Asn Gln Ser
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Leu Gly Gln Ser Ala Pro Ser Leu Thr Ala Gly Leu Lys Glu Leu Ser
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Leu Pro Arg Arg Gly Ser Phe Cys Arg Thr Ser Asn Arg Lys Ser Leu
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Ile Val Thr Ser Ser Thr Ser Pro Thr Leu Pro Arg Pro His Ser Pro
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Leu His Gly His Thr Gly Asn Ser Pro Leu Asp Ser Pro Arg Asn Phe
 195 200 205

Ser Pro Asn Ala Pro Ala His Phe Ser Phe Val Pro Ala Arg Arg Thr
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Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser Ser Gly Tyr Gly
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Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys Ser Ser Gln Glu
 245 250 255

Lys Leu His Gln Leu Pro Phe Gln Pro Thr Ala Asp Glu Leu His Phe
 260 265 270

Leu Thr Lys His Phe Ser Thr Glu Ser Val Pro Asp Glu Glu Gly Arg
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Gln Ser Pro Ala Met Arg Pro Arg Ser Arg Ser Leu Ser Pro Gly Arg
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Ser Pro Val Ser Phe Asp Ser Glu Ile Ile Met Met Asn His Val Tyr
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Lys Glu Arg Phe Pro Lys Ala Thr Ala Gln Met Glu Glu Arg Leu Ala
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Gly Ala Leu Ser Phe Ile His His Gln Val Ile Glu Met Ala Arg Asp
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Cys Leu Asp Lys Ser Arg Ser Gly Leu Ile Thr Ser Gln Tyr Phe Tyr
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Met Ile Ile Ile Ala Arg Pro Ala Arg Leu Leu Glu Cys Leu Glu Phe
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Asp Pro Glu Glu Phe Tyr His Leu Leu Glu Ala Ala Glu Gly His Ala
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Gln Leu Gly Leu Thr Arg Asp Pro Leu Glu Glu Met Ala Gln Leu Ser
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His Gly Ala Ser Leu Pro Ser Lys Lys Thr Pro Ser Glu Glu Asp Phe
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Glu Thr Ile Lys Leu Ile Ser Asn Gly Ala Tyr Gly Ala Val Phe Leu
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Val Arg His Lys Ser Thr Arg Gln Arg Phe Ala Met Lys Lys Ile Asn
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Arg Asp Ile Leu Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Phe
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Cys Ser Phe Asp Thr Lys Arg His Leu Cys Met Val Met Glu Tyr Val
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Val Asp Met Val Arg Leu Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu
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Tyr Leu His Asn Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn
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Ala Arg Lys Gly Ser Tyr Lys Ala Lys Met Ala Arg Arg Ser Lys Arg
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Arg Lys Ile Thr Lys Gln Ala Ser Leu Leu His Thr Ser Arg Ser Leu
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<220>
<223> mouse microtubule associated testis specific
serine/threonine protein kinase (Mtssk, MAST205)

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Asp Ile Phe Ala Pro Thr Gly Lys Val Lys Leu Gln Arg Gln Leu Ser
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Gln Asp Asp Cys Lys Leu Arg Arg Gly Ser Leu Ala Ser Ser Leu Ser
35 40 45

Gly Lys Gln Leu Leu Pro Leu Ser Ser Ser Val His Ser Ser Val Gly
50 55 60

Gln Val Thr Trp Gln Ser Thr Gly Glu Ala Ser Asn Leu Val Arg Met
65 70 75 80

Arg Asn Gln Ser Leu Gly Gln Ser Ala Pro Ser Leu Thr Ala Gly Leu
85 90 95

Lys Glu Leu Ser Leu Pro Arg Arg Gly Ser Phe Cys Arg Thr Ser Asn
100 105 110

Arg Lys Ser Leu Ile Val Thr Ser Ser Thr Ser Pro Thr Leu Pro Arg
115 120 125

Pro His Ser Pro Leu His Gly His Thr Gly Asn Ser Pro Leu Asp Ser
130 135 140

Pro Arg Asn Phe Ser Pro Asn Ala Pro Ala His Phe Ser Phe Val Pro
145 150 155 160

Ala Arg Arg Thr Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser
165 170 175

Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys
180 185 190

Ser Ser Gln Glu Lys Leu His Gln Leu Pro Phe Gln Pro Thr Ala Asp
195 200 205

Glu Leu His Phe Leu Thr Lys His Phe Ser Thr Glu Asn Val Pro Asp
210 215 220

Glu Glu Gly Arg Arg Ser Pro Arg Met Arg Pro Arg Ser Arg Ser Leu
225 230 235 240

Ser Pro Gly Arg Ser Pro Val Ser Phe Asp Ser Glu Ile Ile Met Met
 245 250 255
 Asn His Val Tyr Lys Glu Arg Phe Pro Lys Ala Thr Ala Gln Met Glu
 260 265 270
 Glu Arg Pro Ser Leu Thr Phe Ile Ser Ser Asn Thr Pro Asp Ser Val
 275 280 285
 Leu Pro Leu Ala Asp Gly Ala Leu Ser Phe Ile His His Gln Val Ile
 290 295 300
 Glu Met Ala Arg Asp Cys Leu Asp Lys Ser Arg Ser Gly Leu Ile Thr
 305 310 315 320
 Ser His Tyr Phe Tyr Glu Leu Gln Glu Asn Leu Glu Lys Leu Leu Gln
 325 330 335
 Asp Ala His Glu Arg Ser Glu Ser Ser Asp Val Ala Phe Val Ile Gln
 340 345 350
 Leu Val Lys Lys Leu Met Ile Ile Ala Arg Pro Ala Arg Leu Leu
 355 360 365
 Glu Cys Leu Glu Phe Asp Pro Glu Glu Phe Tyr His Leu Leu Glu Ala
 370 375 380
 Ala Glu Gly His Ala Lys Glu Gly His Gly Ile Lys Cys Asp Ile Pro
 385 390 395 400
 Arg Tyr Ile Val Ser Gln Leu Gly Leu Thr Arg Asp Pro Leu Glu Glu
 405 410 415
 Met Ala Gln Leu Ser Ser Tyr Asp Ser Pro Asp Thr Pro Glu Thr Asp
 420 425 430
 Asp Ser Val Glu Gly Arg Gly Val Ser Gln Pro Ser Gln Lys Thr Pro
 435 440 445
 Ser Glu Glu Asp Phe Glu Thr Ile Lys Leu Ile Ser Asn Gly Ala Tyr
 450 455 460
 Gly Ala Val Phe Leu Val Arg His Lys Ser Thr Arg Gln Arg Phe Ala
 465 470 475 480
 Met Lys Lys Ile Asn Lys Gln Asn Leu Ile Leu Arg Asn Gln Ile Gln
 485 490 495
 Gln Ala Phe Val Glu Arg Asp Ile Leu Thr Phe Ala Glu Asn Pro Phe
 500 505 510
 Val Val Ser Met Phe Cys Ser Phe Glu Thr Lys Arg His Leu Cys Met
 515 520 525
 Val Met Glu Tyr Val Glu Gly Gly Asp Cys Ala Thr Leu Leu Lys Asn
 530 535 540
 Ile Gly Ala Leu Pro Val Asp Met Val Arg Leu Tyr Phe Ala Glu Thr
 545 550 555 560

Val Leu Ala Leu Glu Tyr Leu His Asn Tyr Gly Ile Val His Arg Asp
 565 570 575
 Leu Lys Pro Asp Asn Leu Leu Ile Thr Ser Met Gly His Ile Lys Leu
 580 585 590
 Thr Asp Phe Gly Leu Ser Lys Ile Gly Leu Met Ser Leu Thr Thr Asn
 595 600 605
 Leu Tyr Glu Gly His Ile Glu Lys Asp Ala Arg Glu Phe Leu Asp Lys
 610 615 620
 Gln Val Cys Gly Thr Pro Glu Tyr Ile Ala Pro Glu Val Ile Leu Arg
 625 630 635 640
 Gln Gly Tyr Gly Lys Pro Val Asp Trp Trp Ala Met Gly Ile Ile Leu
 645 650 655
 Tyr Glu Phe Leu Val Gly Cys Val Pro Phe Phe Gly Asp Thr Pro Glu
 660 665 670
 Glu Leu Phe Gly Gln Val Ile Ser Asp Glu Ile Val Trp Pro Glu Gly
 675 680 685
 Asp Asp Ala Leu Pro Pro Asp Ala Gln Asp Leu Thr Ser Lys Leu Leu
 690 695 700
 His Gln Asn Pro Leu Glu Arg Leu Gly Thr Ser Ser Ala Tyr Glu Val
 705 710 715 720
 Lys Gln His Pro Phe Phe Met Gly Leu Asp Trp Thr Gly Leu Leu Arg
 725 730 735
 Gln Lys Ala Glu Phe Ile Pro Gln Leu Glu Ser Glu Asp Asp Thr Ser
 740 745 750
 Tyr Phe Asp Thr Arg Ser Glu Arg Tyr His His Val Asp Ser Glu Asp
 755 760 765
 Glu Glu Glu Val Ser Glu Asp Gly Cys Leu Glu Ile Arg Gln Phe Ser
 770 775 780
 Ser Cys Ser Pro Arg Phe Ser Lys Val Tyr Ser Ser Met Glu Arg Leu
 785 790 795 800
 Ser Leu Leu Glu Glu Arg Arg Thr Pro Pro Pro Thr Lys Arg Ser Leu
 805 810 815
 Ser Glu Glu Lys Glu Asp His Ser Asp Gly Leu Ala Gly Leu Lys Gly
 820 825 830
 Arg Asp Arg Ser Trp Val Ile Gly Ser Pro Glu Ile Leu Arg Lys Arg
 835 840 845
 Leu Ser Val Ser Glu Ser Ser His Thr Glu Ser Asp Ser Ser Pro Pro
 850 855 860
 Met Thr Val Arg His Arg Cys Ser Gly Leu Pro Asp Gly Pro His Cys
 865 870 875 880

Pro Glu Glu Thr Ser Ser Thr Pro Arg Lys Gln Gln Gln Glu Gly Ile
 885 890 895

Trp Val Leu Ile Pro Pro Ser Gly Glu Gly Ser Ser Arg Pro Val Pro
 900 905 910

Glu Arg Pro Leu Glu Arg Gln Leu Lys Leu Asp Glu Glu Pro Pro Gly
 915 920 925

Gln Ser Ser Arg Cys Cys Pro Ala Leu Glu Thr Arg Gly Arg Gly Thr
 930 935 940

Pro Gln Leu Ala Glu Glu Ala Thr Ala Lys Ala Ile Ser Asp Leu Ala
 945 950 955 960

Val Arg Arg Ala Arg His Arg Leu Leu Ser Gly Asp Ser Ile Glu Lys
 965 970 975

Arg Thr Thr Arg Pro Val Asn Lys Val Ile Lys Ser Ala Ser Ala Thr
 980 985 990

Ala Leu Ser Leu Leu Ile Pro Ser Glu His His Ala Cys Ser Pro Leu
 995 1000 1005

Ala Ser Pro Met Ser Pro His Ser Gln Ser Ser Asn Pro Ser Ser Arg
 1010 1015 1020

Asp Ser Ser Pro Ser Arg Asp Phe Leu Pro Ala Leu Gly Ser Leu Arg
 1025 1030 1035 1040

Pro Pro Ile Ile His Arg Ala Gly Lys Lys Tyr Gly Phe Thr Leu
 1045 1050 1055

Arg Ala Ile Arg Val Tyr Met Gly Asp Thr Asp Val Tyr Thr Val His
 1060 1065 1070

His Met Val Trp His Val Glu Asp Gly Gly Pro Ala Ser Glu Ala Gly
 1075 1080 1085

Leu Arg Gln Gly Asp Leu Ile Thr His Val Asn Gly Glu Pro Val His
 1090 1095 1100

Gly Leu Val His Thr Glu Val Val Glu Leu Val Leu Lys Ser Gly Asn
 1105 1110 1115 1120

Lys Val Ser Ile Ser Thr Thr Pro Leu Glu Asn Thr Ser Ile Lys Val
 1125 1130 1135

Gly Pro Ala Arg Lys Gly Ser Tyr Lys Ala Lys Met Ala Arg Arg Ser
 1140 1145 1150

Lys Arg Ser Lys Gly Lys Asp Gly Gln Glu Ser Arg Lys Arg Ser Ser
 1155 1160 1165

Leu Phe Arg Lys Ile Thr Lys Gln Ala Ser Leu Leu His Thr Ser Arg
 1170 1175 1180

Ser Leu Ser Ser Leu Asn Arg Ser Leu Ser Ser Gly Glu Ser Gly Pro
 1185 1190 1195 1200

Gly Ser Pro Thr His Ser His Ser Leu Ser Pro Arg Ser Pro Pro Gln
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 Gly Tyr Arg Val Ala Pro Asp Ala Val His Ser Val Gly Gly Asn Ser
 1220 1225 1230
 Ser Gln Ser Ser Ser Pro Ser Ser Val Pro Ser Ser Pro Ala Gly
 1235 1240 1245
 Ser Gly His Thr Arg Pro Ser Ser Leu His Gly Leu Ala Pro Lys Leu
 1250 1255 1260
 Gln Arg Gln Tyr Arg Ser Pro Arg Arg Lys Ser Ala Gly Ser Ile Pro
 1265 1270 1275 1280
 Leu Ser Pro Leu Ala His Thr Pro Ser Pro Pro Ala Thr Ala Ala Ser
 1285 1290 1295
 Pro Gln Arg Ser Pro Ser Pro Leu Ser Gly His Gly Ser Gln Ser Phe
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 Pro Thr Lys Leu His Leu Ser Pro Pro Leu Gly Arg Gln Leu Ser Arg
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 Pro Lys Ser Ala Glu Pro Pro Arg Ser Pro Leu Leu Lys Arg Val Gln
 1330 1335 1340
 Ser Ala Glu Lys Leu Ala Ala Ala Leu Ala Ala Ala Glu Lys Lys Leu
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 Ala Pro Ser Arg Lys His Ser Leu Asp Leu Pro His Gly Glu Leu Lys
 1365 1370 1375
 Lys Glu Leu Thr Pro Arg Glu Ala Ser Pro Leu Glu Val Val Gly Thr
 1380 1385 1390
 Arg Ser Val Leu Ser Gly Lys Gly Pro Leu Pro Gly Lys Gly Val Leu
 1395 1400 1405
 Gln Pro Ala Pro Ser Arg Ala Leu Gly Thr Leu Arg Gln Asp Arg Ala
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 Glu Arg Arg Glu Ser Leu Gln Lys Gln Glu Ala Ile Arg Glu Val Asp
 1425 1430 1435 1440
 Ser Ser Glu Asp Asp Thr Asp Glu Glu Pro Glu Asn Ser Gln Ala Thr
 1445 1450 1455
 Gln Glu Pro Arg Leu Ser Pro His Pro Glu Ala Ser His Asn Leu Leu
 1460 1465 1470
 Pro Lys Gly Ser Gly Glu Gly Thr Glu Glu Asp Thr Phe Leu His Arg
 1475 1480 1485
 Asp Leu Lys Lys Gln Gly Pro Val Leu Ser Gly Leu Val Thr Gly Ala
 1490 1495 1500
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Val Ser Arg Pro Gln Ala Phe Glu Glu Ala Thr Asn Pro Leu Gln Val
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 Pro Ser Leu Ser Arg Ser Gly Pro Thr Ser Pro Thr Pro Ser Glu Gly
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 Cys Trp Lys Ala Gln His Leu His Thr Gln Ala Leu Thr Ala Leu Cys
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 Pro Ser Phe Ser Glu Leu Thr Pro Thr Gly Cys Ser Ala Ala Thr Ser
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 Thr Ser Gly Lys Pro Gly Thr Trp Ser Trp Lys Phe Leu Ile Glu Gly
 1585 1590 1595 1600

 Pro Asp Arg Ala Ser Thr Asn Lys Thr Ile Thr Arg Lys Gly Glu Pro
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 Ala Asn Ser Gln Asp Thr Asn Thr Thr Val Pro Asn Leu Leu Lys Asn
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 Leu Ser Pro Glu Glu Lys Pro Gln Pro Pro Ser Val Pro Gly Leu
 1635 1640 1645

 Thr His Pro Leu Leu Glu Val Pro Ser Gln Asn Trp Pro Trp Glu Ser
 1650 1655 1660

 Glu Cys Glu Gln Met Glu Lys Glu Glu Pro Ser Leu Ser Ile Thr Glu
 1665 1670 1675 1680

 Val Pro Asp Ser Ser Gly Asp Arg Arg Gln Asp Ile Pro Cys Arg Ala
 1685 1690 1695

 His Pro Leu Ser Pro Glu Thr Arg Pro Ser Leu Leu Trp Lys Ser Gln
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 Glu Leu Gly Gly Gln Gln Asp His Gln Asp Leu Ala Leu Thr Ser Asp
 1715 1720 1725

 Glu Leu Leu Lys Gln Thr
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 <211> 3568
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> human colon Kruppel-like factor (CKLF) cDNA

 <220>
 <221> CDS
 <222> (537)..(1910)
 <223> CKLF

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gttcttcgg cgagggtcgg cggggcggg agcggtcgg ggagagcctg agagcacgg 300
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<212> PRT
<213> Homo sapiens

<220>
<223> human colon Kruppel-like factor (CKLF)

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20 25 30

Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Pro Gly
35 40 45

Glu Glu Leu Lys His Ala His His Arg Pro Gln Ala Gln Pro Ala Pro
50 55 60

Ala Gln Ala Pro Gln Pro Ala Gln Pro Pro Ala Thr Gly Pro Arg Leu
65 70 75 80

Pro Pro Glu Asp Leu Val Gln Thr Arg Cys Glu Met Glu Lys Tyr Leu
85 90 95

Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Pro Glu His Lys Lys Tyr
100 105 110

Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe Phe Thr Asp Thr Glu
115 120 125

Gly Leu Pro Tyr Ser Ile Asn Met Asn Val Phe Leu Pro Asp Ile Thr
130 135 140

His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg Pro Cys Val Thr His
145 150 155 160

Ile Lys Thr Glu Pro Val Ala Ile Phe Ser His Gln Ser Glu Thr Thr
165 170 175

Ala Pro Pro Pro Ala Pro Thr Gln Ala Leu Pro Glu Phe Thr Ser Ile
180 185 190

Phe Ser Ser His Gln Thr Ala Ala Pro Glu Val Asn Asn Ile Phe Ile
195 200 205

Lys Gln Glu Leu Pro Thr Pro Asp Leu His Leu Ser Val Pro Thr Gln
210 215 220

Gln Gly His Leu Tyr Gln Leu Leu Asn Thr Pro Asp Leu Asp Met Pro
225 230 235 240

Ser Ser Thr Asn Gln Thr Ala Ala Met Asp Thr Leu Asn Val Ser Met
245 250 255

Ser Ala Ala Met Ala Gly Leu Asn Thr His Thr Ser Ala Val Pro Gln
260 265 270

Thr Ala Val Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr Thr Met
275 280 285

Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro Ser Pro
290 295 300

Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met Leu Gln
305 310 315 320

Asn Leu Thr Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser Lys Leu
325 330 335

Ala Ile His Asn Pro Asn Leu Pro Thr Thr Leu Pro Val Asn Ser Gln
340 345 350

Asn Ile Gln Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp Leu Glu
355 360 365

Lys Arg Arg Ile His Tyr Cys Asp Tyr Pro Gly Cys Thr Lys Val Tyr
370 375 380

Thr Lys Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr Gly Glu
385 390 395 400

Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp Trp Arg Phe Ala Arg
405 410 415

Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala Lys Pro
420 425 430

Phe Gln Cys Gly Val Cys Asn Arg Ser Phe Ser Arg Ser Asp His Leu
435 440 445

Ala Leu His Met Lys Arg His Gln Asn
450 455

<210> 35

<211> 1591

<212> DNA

<213> Mus musculus

<220>

<223> mouse intestinal-enriched Kruppel-like factor
(IKLF, CKLF) cDNA

<220>

<221> CDS

<222> (167)..(1507)

<223> CKLF

<400> 35

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 cttaaaccg cagacctaacttcataaaaaa g 1591

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 <212> PRT
 <213> *Mus musculus*

<220>
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 (IKLF, CKLF)

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 Met Pro Thr Arg Val Leu Thr Met Ser Ala Arg Leu Gly Pro Leu Pro
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 Gln Pro Pro Ala Ala Gln Ala Glu Pro Val Phe Ala Gln Leu Lys Pro
 20 25 30

 Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Ser Gly
 35 40 45

 Asp Asp Leu Lys His Ala His His Pro Pro Ala Pro Pro Pro Ala
 50 55 60

 Ala Gly Pro Arg Leu Pro Ser Glu Glu Leu Val Gln Thr Arg Cys Glu
 65 70 75 80

 Met Glu Lys Tyr Leu Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Ser
 85 90 95

 Glu His Lys Lys Tyr Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe
 100 105 110

 Phe Thr Asp Thr Glu Gly Ile Pro Tyr Ser Ile Asn Met Asn Val Phe
 115 120 125

 Leu Pro Asp Ile Thr His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg
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 Pro Cys Val Thr Gln Ile Lys Thr Glu Pro Val Thr Ile Phe Ser His
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Gln Ser Glu Ser Thr Ala Pro Pro Pro Pro Pro Ala Pro Thr Gln Ala
 165 170 175 ·
 Leu Pro Glu Phe Thr Ser Ile Phe Ser Ser His Gln Thr Thr Ala Pro
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 Pro Gln Glu Val Asn Asn Ile Phe Ile Lys Gln Glu Leu Pro Ile Pro
 195 200 205
 Asp Leu His Leu Ser Val Pro Ser Gln Gln Gly His Leu Tyr Gln Leu
 210 215 220
 Leu Asn Thr Pro Asp Leu Asp Met Pro Ser Ser Thr Asn Gln Thr Ala
 225 230 235 240
 Val Met Asp Thr Leu Asn Val Ser Met Ala Gly Leu Asn Pro His Pro
 245 250 255
 Ser Ala Val Pro Gln Thr Ser Met Lys Gln Phe Gln Gly Met Pro Pro
 260 265 270
 Cys Thr Tyr Thr Met Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr
 275 280 285
 Phe Pro Pro Ser Pro Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln
 290 295 300
 Ala Glu Met Leu Gln Asn Leu Thr Pro Pro Pro Ser Tyr Ala Ala Thr
 305 310 315 320
 Ile Ala Ser Lys Leu Ala Ile His Asn Pro Asn Leu Pro Ala Thr Leu
 325 330 335
 Pro Val Asn Ser Pro Thr Leu Pro Pro Val Arg Tyr Asn Arg Arg Ser
 340 345 350
 Asn Pro Asp Leu Glu Lys Arg Arg Ile His Phe Cys Asp Tyr Asn Gly
 355 360 365
 Cys Thr Lys Val Tyr Thr Lys Ser Ser His Leu Lys Ala His Leu Arg
 370 375 380
 Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp
 385 390 395 400
 Trp Arg Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His
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 Thr Gly Ala Lys Pro Phe Gln Cys Met Val Cys Gln Arg Ser Phe Ser
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 Arg Ser Asp His Leu Ala Leu His Met Lys Arg His Gln Asn
 435 440 445

<210> 37
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 <212> DNA
 <213> Rattus norvegicus

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<223> rat Kruppel-like factor 5, intestinal (KLF5, CKLF)
CDNA

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<400> 37

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<210> 38

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<400> 38

Ser Met Ala Gly Leu Asn Ser His Pro Ser Ala Val Pro Gln Thr Ser
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Met Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr Thr Met Pro Ser
35 40 45

Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro Pro Ser Pro Pro Ser
 50 55 60

Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met Leu Gln Asn Leu
65 70 75 80

Thr Pro Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser Lys Leu Ala Ile
85 90 95

His Asn Pro Asn Leu Pro Ala Thr Leu Pro Val Asn Ser Pro Asn Ile
100 105 110

Gln Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp Leu Glu Lys Arg
115 120 125

Arg Ile His Phe Cys Asp Tyr Asp Gly Cys Thr Lys Val Tyr Thr Lys
130 135 140
Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr Gly Glu Lys Pro
145 150 155 160
Tyr Lys Cys Thr Trp Glu Gly Cys Asp Trp Arg Phe Ala Arg Ser Asp
165 170 175
Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala Lys Pro Phe Gln
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Cys Val Val Cys Asn Arg Ser Phe Ser Arg Ser Asp His Leu Ala Leu
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<212> DNA
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Taqman Probe Probe133

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Forward primer 717F

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<210> 44
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<212> DNA
<213> Artificial Sequence

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(His) affinity tag

<400> 45
His His His His His His
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<210> 46
<211> 200
<212> PRT
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<220>
<223> Description of Artificial Sequence:poly-Gly
flexible linker

<220>
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<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
or absent

<400> 46
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1 5 10 15

Gly
20 25 30

Gly
35 40 45

Gly
50 55 60

Gly
65 70 75 80

Gly
85 90 95

Gly
100 105 110

Gly
115 120 125

Gly
130 135 140

Gly
145 150 155 160

Gly
165 170 175

Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly
195 200